

IN THE CLAIMS

Amend the claims as follows.

Claims 1-114 (Canceled).

115. (new) An isolated nucleic acid sequence comprising a 16S-23S rRNA spacer sequence selected from the group consisting of: SEQ ID NO:111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, a sequence complementary to any of the above-recited sequences; and a sequence recited above which contains a U in place of T.

116. (new) An isolated nucleic acid sequence according to claim 115, wherein said nucleic acid sequence consists of a 16S-23S rRNA spacer sequence selected from the group consisting of: SEQ ID NO:111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, a sequence complementary to any of the above-recited sequences; and a sequence recited above which contains a U in place of T.

117. (new) Method for the detection and identification of one *Pseudomonas* species, or for the simultaneous detection of several *Pseudomonas* species in a sample, comprising the steps of:

(i) optionally releasing, isolating and/or concentrating the polynucleic acids to be detected in the sample;

(ii) optionally amplifying the 16S-23S rRNA spacer region, or a part thereof, with at least one primer pair;

(iii) detecting the presence of a nucleic acid according to claim 116;

(iv) identifying the *Pseudomonas* species present in said sample from the nucleic acid(s) detected in said sample.

118. (new) Method according to claim 117 wherein said detecting comprises sequence analysis of said nucleic acid(s).

119. (new) A composition comprising a diluent and a sequencing primer that specifically hybridizes with a 16S-23S rRNA spacer sequence of claim 116.

120. (new) . A kit for the detection and identification of at least one *Pseudomonas* species, or for the simultaneous detection and identification of several *Pseudomonas* species in a sample comprising a composition according to claim 119.

121. (new) Method according to claim 117 wherein said detecting comprises specifically hybridizing at least one probe to said nucleic acid.

122. (new) A composition comprising a diluent and at least one probe that specifically hybridizes with a 16S-23S rRNA spacer sequence of claim 116.

123. (new) A kit for the detection and identification of at least one *Pseudomonas* species, or for the simultaneous detection and identification of several *Pseudomonas* species in a sample comprising the following components:

- (i) optionally, at least one primer pair allowing amplification of a 16S-23S rRNA spacer region, or a part thereof;
- (ii) a composition according to claim 122;
- (iii) optionally, a buffer, or components necessary to produce the buffer, enabling a hybridization reaction between a probe of (ii) and a nucleic acid present in a sample, or amplified products thereof;
- (v) optionally, a solution, or components necessary for producing the solution, enabling washing of hybrids formed under the appropriate wash conditions;
- (vi) optionally, a means for detecting the hybrids resulting from hybridization.

124. (new) Method according to claim 117 for the detection and identification of *Pseudomonas aeruginosa* wherein said nucleic acid of step (iii) is a sequence consisting of SEQ ID NO 111.

125. (new) Method according to claim 117 for the detection and identification of *Pseudomonas pseudoalcaligenes* wherein said nucleic acid of step (iii) is a sequence consisting of SEQ ID NO 112.

126. (new) Method according to claim 117 for the detection and identification of *Pseudomonas stutzeri* wherein said nucleic acid of step (iii) is a sequence consisting of SEQ ID NO 113.

127. (new) Method according to claim 117 for the detection and identification of *Pseudomonas alcaligenes* wherein said nucleic acid of step (iii) is sequence consisting of SEQ ID NO 114.

128. (new) Method according to claim 117 for the detection and identification of *Pseudomonas putida* wherein said nucleic acid of step (iii) is sequence consisting of SEQ ID NO 115.

129. (new) An isolated 16S-23S rRNA spacer probe nucleic acid sequence comprising a first nucleic acid sequence, said probe specifically hybridizing to a second nucleic acid sequence, said second nucleic acid sequence being selected from the group consisting of: SEQ ID NO:111, SEQ ID NO:111 containing a U in place of T, a sequence complementary to SEQ ID NO:111, a sequence complementary to SEQ ID NO:111 containing a U in place of T, SEQ ID NO:112, SEQ ID NO:112 containing a U in place of T, a sequence complementary to SEQ ID NO:112, a sequence complementary to SEQ ID NO:112 containing a U in place of T, SEQ ID NO:113, SEQ ID NO:113 containing a U in place of T, a sequence complementary to SEQ ID NO:113, a sequence complementary to SEQ ID NO:113 containing a U in place of T, SEQ ID NO:114, SEQ ID NO:114 containing a U in place of T, a sequence complementary to SEQ ID NO:114, a sequence complementary to SEQ ID NO:114 containing a U in place of T, SEQ ID NO:115, SEQ ID NO:115 containing a U in place of T, a sequence complementary to SEQ ID NO:115, and a sequence complementary to SEQ ID NO:115 containing a U in place of T .

130. (new) The probe of a claim 129 wherein the first nucleic acid sequence is at least 5-200 nucleotides in length.

131. (new) The probe of a claim 129 wherein the first nucleic acid sequence is at least 5-50 nucleotides in length.

132. (new) The probe of a claim 129 wherein the first nucleic acid sequence is at least 10-25 nucleotides in length.

133. (new) The probe of claim 129 wherein said probe specifically hybridizes to said second nucleic acid sequence in a medium containing 3xSSC and 20% formamide, at a temperature in the range of 45°C to 55°C.

134. (new) A probe of claim 129 wherein said probe is a nucleic acid sequence consisting of said first nucleic acid sequence.

135. (new) Method for the detection and identification of one *Pseudomonas* species, or for the simultaneous detection of several *Pseudomonas* species in a sample, comprising the steps of:

(i) optionally releasing, isolating and/or concentrating the polynucleic acids to be detected in the sample;

(ii) optionally amplifying the 16S-23S rRNA spacer region, or a part thereof, with at least one primer pair;

(iii) detecting the presence of a nucleic acid sequence selected from the group consisting of: SEQ ID NO:111, SEQ ID NO:111 containing a U in place of T, a sequence complementary to SEQ ID NO:111, a sequence complementary to SEQ ID NO:111 containing a U in place of T, SEQ ID NO:112, SEQ ID NO:112 containing a U in place of T, a sequence complementary to SEQ ID NO:112, a sequence complementary to SEQ ID NO:112 containing a U in place of T, SEQ ID NO:113, SEQ ID NO:113 containing a U in place of T, a sequence complementary to SEQ ID NO:113, a sequence complementary to SEQ ID NO:113 containing a U in place of T, SEQ ID NO:114, SEQ ID NO:114 containing a U in place of T, a sequence complementary to SEQ ID NO:114, a sequence complementary to SEQ ID NO:114 containing a U in place of T, SEQ ID NO:115, SEQ ID NO:115 containing a U in place of T, a sequence complementary to SEQ ID NO:115, and a sequence complementary to SEQ ID NO:115 containing a U in place of T ; and

(iv) identifying the *Pseudomonas* species present in said sample from the nucleic acid(s) detected in said sample.

136. (new) Method according to claim 135 wherein said detecting comprises sequence analysis of said nucleic acid sequence.

137. (new) A composition comprising a diluent and a sequencing primer that specifically hybridizes with a nucleic acid sequence selected from the group consisting of: SEQ ID NO:111, SEQ ID NO:111 containing a U in place of T, a sequence complementary to SEQ ID NO:111, a sequence complementary to SEQ ID NO:111

containing a U in place of T, SEQ ID NO:112, SEQ ID NO:112 containing a U in place of T, a sequence complementary to SEQ ID NO:112, a sequence complementary to SEQ ID NO:112 containing a U in place of T, SEQ ID NO:113, SEQ ID NO:113 containing a U in place of T, a sequence complementary to SEQ ID NO:113, a sequence complementary to SEQ ID NO:113 containing a U in place of T, SEQ ID NO:114, SEQ ID NO:114 containing a U in place of T, a sequence complementary to SEQ ID NO:114, a sequence complementary to SEQ ID NO:114 containing a U in place of T, SEQ ID NO:115, SEQ ID NO:115 containing a U in place of T, a sequence complementary to SEQ ID NO:115, and a sequence complementary to SEQ ID NO:115 containing a U in place of T .

138. (new) A kit for the detection and identification of at least one *Pseudomonas* species, or for the simultaneous detection and identification of several *Pseudomonas* species in a sample comprising a diluent and a probe of claim 129.

139. (new) Method for the detection and identification of one *Pseudomonas* species, or for the simultaneous detection of several *Pseudomonas* species in a sample, comprising the steps of:

(i) optionally releasing, isolating and/or concentrating the polynucleic acids to be detected in the sample;

(ii) optionally amplifying the 16S-23S rRNA spacer region, or a part thereof, with at least one primer pair;

(iii) detecting the presence of a *Pseudomonas* specific nucleic acid sequence by hybridizing a probe of claim 129 to any *Pseudomonas* specific nucleic acid sequence present in said sample; and

(iv) identifying the *Pseudomonas* species present in said sample from the nucleic acid(s) detected in said sample.

140. (new) A kit for the detection and identification of at least one *Pseudomonas* species, or for the simultaneous detection and identification of several *Pseudomonas* species in a sample comprising the following components:

(i) optionally, at least one primer pair allowing amplification of a 16S-23S rRNA spacer region, or a part thereof;

(ii) a composition comprising a diluent and a probe of claim 129;

(iii) optionally, a buffer, or components necessary to produce the buffer, enabling a hybridization reaction between a probe of (ii) and a nucleic acid present in a sample, or amplified products thereof;

(v) optionally, a solution, or components necessary for producing the solution, enabling washing of hybrids formed under the appropriate wash conditions;

(vi) optionally, a means for detecting the hybrids resulting from hybridization.

141. (new) Method according to claim 135 for the detection and identification of *Pseudomonas aeruginosa* wherein said nucleic acid sequence is a sequence selected from the group consisting of: SEQ ID NO:111, a sequence complementary to SEQ ID

NO:111, SEQ ID NO:111 which contains a U in place of T; and a sequence complementary to SEQ ID NO:111 which contains a U in place of T.

142. (new) Method according to claim 135 for the detection and identification of *Pseudomonas pseudoalcaligenes* wherein said nucleic acid sequence is a sequence selected from the group consisting of: SEQ ID NO:112, a sequence complementary to SEQ ID NO:112, SEQ ID NO:112 which contains a U in place of T; and a sequence complementary to SEQ ID NO:112 which contains a U in place of T.

143. (new) Method according to claim 135 for the detection and identification of *Pseudomonas stutzeri* wherein said nucleic acid sequence is a sequence selected from the group consisting of: SEQ ID NO:113, a sequence complementary to SEQ ID NO:113, SEQ ID NO:113 which contains a U in place of T; and a sequence complementary to SEQ ID NO:113 which contains a U in place of T.

144. (new) Method according to claim 135 for the detection and identification of *Pseudomonas alcaligenes* wherein said nucleic acid sequence is a sequence selected from the group consisting of: SEQ ID NO:114, a sequence complementary to SEQ ID NO:114, SEQ ID NO:114 which contains a U in place of T; and a sequence complementary to SEQ ID NO:114 which contains a U in place of T.

145. (new) Method according to claim 135 for the detection and identification of *Pseudomonas putida* wherein said nucleic acid sequence is a sequence selected from

the group consisting of: SEQ ID NO:115, a sequence complementary to SEQ ID NO:115, SEQ ID NO:115 which contains a U in place of T; and a sequence complementary to SEQ ID NO:115 which contains a U in place of T.

146. (new) An isolated nucleic acid sequence, said nucleic acid sequence consisting of 5-1000 nucleic acids, said 5-1000 nucleic acids comprising at least 5-200 contiguous nucleic acids of a nucleic acid sequence selected from the group consisting of: SEQ ID NO:111, SEQ ID NO:111 containing a U in place of T, a sequence complementary to SEQ ID NO:111, a sequence complementary to SEQ ID NO:111 containing a U in place of T, SEQ ID NO:112, SEQ ID NO:112 containing a U in place of T, a sequence complementary to SEQ ID NO:112, a sequence complementary to SEQ ID NO:112 containing a U in place of T, SEQ ID NO:113, SEQ ID NO:113 containing a U in place of T, a sequence complementary to SEQ ID NO:113, a sequence complementary to SEQ ID NO:113 containing a U in place of T, SEQ ID NO:114, SEQ ID NO:114 containing a U in place of T, a sequence complementary to SEQ ID NO:114, a sequence complementary to SEQ ID NO:114 containing a U in place of T, SEQ ID NO:115, SEQ ID NO:115 containing a U in place of T, a sequence complementary to SEQ ID NO:115, and a sequence complementary to SEQ ID NO:115 containing a U in place of T.

147. (new) A probe of claim 129 further comprising a detectable label.

148. (new) A probe of claim 146 further comprising a detectable label.

149. (new) An isolated nucleic acid sequence comprising a 16S-23S rRNA spacer sequence selected from the group consisting of: SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, a sequence complementary to any of the above-recited sequences; and a sequence recited above which contains a U in place of T.

150. (new) An isolated nucleic acid sequence selected from the group consisting of SEQ ID NO:111, SEQ ID NO:115, a sequence complementary to SEQ ID NO:111 or SEQ ID NO:115, and a sequence recited above which contains a U in place of T.